

WO 2005/040191

PCT/US2004/019766

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lau, Lester F.
- (ii) TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
  - (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
  - (C) CITY: Chicago
  - (D) STATE: Illinois
  - (E) COUNTRY: United States of America
  - (F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Clough, David W.
  - (B) REGISTRATION NUMBER: 36,107
  - (C) REFERENCE/DOCKET NUMBER: 28758/33766
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 312/474-6300
  - (B) TELEFAX: 312/474-0448
  - (C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1480 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 180..1316
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (D) OTHER INFORMATION: "Mouse cyr61 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGAGCGCC CCAGAGAAGC GCCTGCAATC TCTGCGCCTC CTCCGCCAGC ACCTCGAGAG 60  
 AAGGACACCC GCCGCCTCGG CCCTCGCCTC ACCGCACTCC GGGCGCATTT GATCCCGCTG 120

WO 2005/040191

PCT/US2004/019766

CTCGCCGGCT TGTTGGTTCT GTGTCGCCGC GTCGCCCCG GTTCCTCTG CGCGCCACA	179
ATG-AGC TCC AGC ACC TTC AGG ACG CTC GCT GTC GCC GTC ACC CTT CTC Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu 1 5 10 15	227
CAC TTG ACC AGA CTG GCG CTC TCC ACC TGC CCC GCC GCC TGC CAC TGC His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys 20 25 30	275
CCT CTG GAG GCA CCC AAG TGC GCC CCG GGA GTC GGG TTG GTC CGG GAC Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp 35 40 45	323
GGC TGC GGC TGC TGT AAG GTC TGC GCT AAA CAA CTC AAC GAG GAC TGC Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys 50 55 60	371
AGC AAA ACT CAG CCC TGC GAC CAC ACC AAG GGG TTG GAA TGC AAT TTC Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe 65 70 75 80	419
GGC GCC AGC TCC ACC GCT CTG AAA GGG ATC TGC AGA GCT CAG TCA GAA Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu 85 90 95	467
GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA AGC Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser 100 105 110	515
TTC CAG CCC AAC TGT AAA CAC CAG TGC ACA TGT ATT GAT GGC GCC GTG Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val 115 120 125	563
GGC TGC ATT CCT CTG TGT CCC CAA GAA CTG TCT CTC CCC AAT CTG GGC Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly 130 135 140	611
TGT CCC AAC CCC CGG CTG GTG AAA GTC AGC GGG CAG TGC TGT GAA GAG Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu 145 150 155 160	659
TGG GTT TGT GAT GAA GAC AGC ATT AAG GAC TCC CTG GAC GAC CAG GAT Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp 165 170 175	707
GAC CTC CTC GGA CTC GAT GCC TCG GAG GTG GAG TTA ACG AGA AAC AAT Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn 180 185 190	755
GAG TTA ATC GCA ATT GGA AAA GGC AGC TCA CTG AAG AGG CTT CCT GTC Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val 195 200 205	803
TTT GGC ACC GAA CCG CGA GTT CTT TTC AAC CCT CTG CAC GCC CAT GGC Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly 210 215 220	851
CAG AAA TGC ATC GTT CAG ACC ACG TCT TGG TCC CAG TGC TCC AAG AGC Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser 225 230 235 240	899
TGC GGA ACT GGC ATC TCC ACA CGA GTT ACC AAT GAC AAC CCA GAG TGC	947

Cys	Gly	Thr	Gly	Ile	Ser	Thr	Arg	Val	Thr	Asn	Asp	Asn	Pro	Glu	Cys	
245				245				250						255		
CGC	CTG	GTG	AAA	GAG	ACC	CGG	ATC	TGT	GAA	GTG	CGT	CCT	TGT	GGA	CAA	995
Arg	Leu	Val	Lys	Glu	Thr	Arg	Ile	Cys	Glu	Val	Arg	Pro	Cys	Gly	Gln	
			260					265						270		
CCA	GTG	TAC	AGC	AGC	CTA	AAA	AAG	GGC	AAG	AAA	TGC	AGC	AAG	ACC	AAG	1043
Pro	Val	Tyr	Ser	Ser	Leu	Lys	Lys	Gly	Lys	Lys	Cys	Ser	Lys	Thr	Lys	
			275					280					285			
AAA	TCC	CCA	GAA	CCA	GTC	AGA	TTT	ACT	TAT	GCA	GGA	TGC	TCC	AGT	GTC	1091
Lys	Ser	Pro	Glu	Pro	Val	Arg	Phe	Thr	Tyr	Ala	Gly	Cys	Ser	Ser	Val	
			290					295				300				
AAG	AAA	TAC	CGG	CCC	AAA	TAC	TGC	GGC	TCC	TGC	GTA	GAT	GGC	CGG	TGC	1139
Lys	Lys	Tyr	Arg	Pro	Lys	Tyr	Cys	Gly	Ser	Cys	Val	Asp	Gly	Arg	Cys	
			305			310				315				320		
TGC	ACA	CCT	CTG	CAG	ACC	AGA	ACT	GTG	AAG	ATG	CGG	TTC	CGA	TGC	GAA	1187
Cys	Thr	Pro	Leu	Gln	Thr	Arg	Thr	Val	Lys	Met	Arg	Phe	Arg	Cys	Glu	
				325					330					335		
GAT	GGA	GAG	ATG	TTT	TCC	AAG	AAT	GTC	ATG	ATG	ATC	CAG	TCC	TGC	AAA	1235
Asp	Gly	Glu	Met	Phe	Ser	Lys	Asn	Val	Met	Met	Ile	Gln	Ser	Cys	Lys	
			340					345					350			
TGT	AAC	TAC	AAC	TGC	CCG	CAT	CCC	AAC	GAG	GCA	TCG	TTC	CGA	CTG	TAC	1283
Cys	Asn	Tyr	Asn	Cys	Pro	His	Pro	Asn	Glu	Ala	Ser	Phe	Arg	Leu	Tyr	
			355				360					365				
AGC	CTA	TTC	AAT	GAC	ATC	CAC	AAG	TTC	AGG	GAC	TAAGTGCCTC	CAGGGTTCCT				1336
Ser	Leu	Phe	Asn	Asp	Ile	His	Lys	Phe	Arg	Asp						
			370				375									
AGTGTGGGCT	GGACAGAGGA	GAAGCGCAAG	CATCATGGAG	ACGTGGGTGG	GCGGAGGATG											1396
AATGGTGCCT	TGCTCATTCT	TGAGTAGCAT	TAGGGTATTT	CAAACTGCC	AAGGGGCTGA											1456
TGTGGACGGA	CAGCAGCGCA	GCCG														1480

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (D) OTHER INFORMATION: "Mouse Cyr61 amino acid sequence"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ser	Ser	Thr	Phe	Arg	Thr	Leu	Ala	Val	Ala	Val	Thr	Leu	Leu	
1				5					10					15		
His	Leu	Thr	Arg	Leu	Ala	Leu	Ser	Thr	Cys	Pro	Ala	Ala	Cys	His	Cys	
			20					25					30			
Pro	Leu	Glu	Ala	Pro	Lys	Cys	Ala	Pro	Gly	Val	Gly	Leu	Val	Arg	Asp	

35 40 45  
 Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys  
 50 55 60  
 Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe  
 65 70 75 80  
 Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu  
 85 90 95  
 Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser  
 100 105 110  
 Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val  
 115 120 125  
 Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly  
 130 135 140  
 Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu  
 145 150 155 160  
 Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp  
 165 170 175  
 Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn  
 180 185 190  
 Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val  
 195 200 205  
 Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly  
 210 215 220  
 Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser  
 225 230 235 240  
 Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys  
 245 250 255  
 Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln  
 260 265 270  
 Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys  
 275 280 285  
 Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val  
 290 295 300  
 Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys  
 305 310 315 320  
 Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu  
 325 330 335  
 Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys  
 340 345 350  
 Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr  
 355 360 365  
 Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp

370

375

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 124..1266

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (D) OTHER INFORMATION: "Human cyr61 cDNA coding sequence"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

GGGCGGGCCC ACCGCGACAC CGCGCCGCCA CCCCAGCCCC GCTGCGCACG GCCTGTCCGC      60
TGCACACCAG CTGTGTGGCG TCCTCGTCGC CGCGCTCGCC CCGGGCTACT CCTGCGCGCC      120
ACA ATG AGC TCC CGC ATC GCC AGG GCG CTC GCC TTA GTC GTC ACC CTT      168
  Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu
    1             5             10             15
CTC CAC TTG ACC AGG CTG GCG CTC TCC ACC TGC CCC GCT GCC TGC CAC      216
Leu His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His
          20             25             30
TGC CCC CTG GAG GCG CCC AAG TGC GCG CCG GGA GTC GGG CTG GTC CGG      264
Cys Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg
          35             40             45
GAC GGC TGC GGC TGC TGT AAG GTC TGC GCC AAG CAG CTC AAC GAG GAG      312
Asp Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp
          50             55             60
TGC AGC AAA ACG CAG CCC TGC GAC CAC ACC AAG GGG CTG GAA TGC AAC      360
Cys Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn
          65             70             75
TTC GGC GCC AGC TCC ACC GCT CTG AAG GGG ATC TGC AGA GCT CAG TCA      408
Phe Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser
          80             85             90             95
GAG GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA      456
Glu Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu
          100            105            110
AGT TTC CAG CCC AAC TGT CAA CAT CAG TGC ACA TGT ATT GAT GGC GCC      504
Ser Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala
          115            120            125
GTG GGC TGC ATT CCT CTG TGT CCC CAA GAA CTA TCT CTC CCC AAC TTG      552
Val Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu
          130            135            140
GGC TGT CCC AAC CCT CGG CTG GTC AAA GTT ACC GGG CAG TGC TGC GAG      600

```

Gly	Cys	Pro	Asn	Pro	Arg	Leu	Val	Lys	Val	Thr	Gly	Gln	Cys	Cys	Glu	
145						150					155					
GAG	TGG	GTC	TGT	GAC	GAG	GAT	AGT	ATC	AAG	GAC	CCC	ATG	GAG	GAC	CAG	648
Glu	Trp	Val	Cys	Asp	Glu	Asp	Ser	Ile	Lys	Asp	Pro	Met	Glu	Asp	Gln	
160					165					170					175	
GAC	GGC	CTC	CTT	GGC	AAG	GAG	CTG	GGA	TTC	GAT	GCC	TCC	GAG	GTG	GAG	696
Asp	Gly	Leu	Leu	Gly	Lys	Glu	Leu	Gly	Phe	Asp	Ala	Ser	Glu	Val	Glu	
				180					185					190		
TTG	ACG	AGA	AAC	AAT	GAA	TTG	ATT	GCA	GTT	GGA	AAA	GGC	AGA	TCA	CTG	744
Leu	Thr	Arg	Asn	Asn	Glu	Leu	Ile	Ala	Val	Gly	Lys	Gly	Arg	Ser	Leu	
			195					200					205			
AAG	CGG	CTC	CCT	GTT	TTT	GGA	ATG	GAG	CCT	CGC	ATC	CTA	TAC	AAC	CCT	792
Lys	Arg	Leu	Pro	Val	Phe	Gly	Met	Glu	Pro	Arg	Ile	Leu	Tyr	Asn	Pro	
	210					215						220				
TTA	CAA	GGC	CAG	AAA	TGT	ATT	GTT	CAA	ACA	ACT	TCA	TGG	TCC	CAG	TGC	840
Leu	Gln	Gly	Gln	Lys	Cys	Ile	Val	Gln	Thr	Thr	Ser	Trp	Ser	Gln	Cys	
	225					230					235					
TCA	AAG	ACC	TGT	GGA	ACT	GGT	ATC	TCC	ACA	CGA	GTT	ACC	AAT	GAC	AAC	888
Ser	Lys	Thr	Cys	Gly	Thr	Gly	Ile	Ser	Thr	Arg	Val	Thr	Asn	Asp	Asn	
240					245					250					255	
CCT	GAG	TGC	CGC	CTT	GTG	AAA	GAA	ACC	CGG	ATT	TGT	GAG	GTG	CGG	CCT	936
Pro	Glu	Cys	Arg	Leu	Val	Lys	Glu	Thr	Arg	Ile	Cys	Glu	Val	Arg	Pro	
				260					265					270		
TGT	GGA	CAG	CCA	GTG	TAC	AGC	AGC	CTG	AAA	AAG	GGC	AAG	AAA	TGC	AGC	984
Cys	Gly	Gln	Pro	Val	Tyr	Ser	Ser	Leu	Lys	Lys	Gly	Lys	Lys	Cys	Ser	
			275					280					285			
AAG	ACC	AAG	AAA	TCC	CCC	GAA	CCA	GTC	AGG	TTT	ACT	TAC	GCT	GGA	TGT	1032
Lys	Thr	Lys	Lys	Ser	Pro	Glu	Pro	Val	Arg	Phe	Thr	Tyr	Ala	Gly	Cys	
	290					295						300				
TTG	AGT	GTG	AAG	AAA	TAC	CGG	CCC	AAG	TAC	TGC	GGT	TCC	TGC	GTG	GAC	1080
Leu	Ser	Val	Lys	Lys	Tyr	Arg	Pro	Lys	Tyr	Cys	Gly	Ser	Cys	Val	Asp	
	305					310					315					
GGC	CGA	TGC	TGC	ACG	CCC	CAG	CTG	ACC	AGG	ACT	GTG	AAG	ATG	CGG	TTC	1128
Gly	Arg	Cys	Cys	Thr	Pro	Gln	Leu	Thr	Arg	Thr	Val	Lys	Met	Arg	Phe	
320					325					330					335	
CGC	TGC	GAA	GAT	GGG	GAG	ACA	TTT	TCC	AAG	AAC	GTC	ATG	ATG	ATC	CAG	1176
Arg	Cys	Glu	Asp	Gly	Glu	Thr	Phe	Ser	Lys	Asn	Val	Met	Met	Ile	Gln	
				340					345					350		
TCC	TGC	AAA	TGC	AAC	TAC	AAC	TGC	CCG	CAT	GCC	AAT	GAA	GCA	GCG	TTT	1224
Ser	Cys	Lys	Cys	Asn	Tyr	Asn	Cys	Pro	His	Ala	Asn	Glu	Ala	Ala	Phe	
			355					360					365			
CCC	TTC	TAC	AGG	CTG	TTC	AAT	GAC	ATT	CAC	AAA	TTT	AGG	GAC			1266
Pro	Phe	Tyr	Arg	Leu	Phe	Asn	Asp	Ile	His	Lys	Phe	Arg	Asp			
		370				375						380				
TAAATGCTAC	CTGGGTTTCC	AGGGCACACC	TAGACAAACA	AGGGAGAAGA	GTGTCAGAAT											1326
CAGAATCATG	GAGAAAATGG	GCGGGGGTGG	TGTGGGTGAT	GGGACTCATT	G TAGAAAGGA											1386

AGCCTTCTCA TTCTTGAGGA GCATTAAGGT AT

1418

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (D) OTHER INFORMATION: "Human Cyr61 amino acid sequence"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu Leu
 1           5           10           15
His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
 20           25           30
Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
 35           40           45
Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
 50           55           60
Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
 65           70           75           80
Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
 85           90           95
Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
100          105          110
Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala Val
115          120          125
Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
130          135          140
Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu Glu
145          150          155          160
Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln Asp
165          170          175
Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu Leu
180          185          190
Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu Lys
195          200          205
Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro Leu
210          215          220
Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser
225          230          235          240
Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro

```

	245		250		255
Glu Cys Arg	Leu Val Lys Glu Thr-Arg-Ile Cys Glu Val Arg Pro Cys				
	260		265		270
Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys					
	275		280		285
Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Leu					
	290		295		300
Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly					
	305		310		315
Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe Arg					
	325		330		335
Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln Ser					
	340		345		350
Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe Pro					
	355		360		365
Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp					
	370		375		380

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (D) OTHER INFORMATION: "Fispl2 cDNA coding sequence"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGCC GACAACCCCA GACGCCACCG CCTGGAGCGT CCAGACACCA ACCTCCGCCC	60
CTGTCCGAAT CCAGGCTCCA GCCGCGCCTC TCGTCGCCTC TGCACCCTGC TGTGCATCCT	120
CCTACCGCGT CCCGATCATG CTCGCCTCCG TCGCAGGTCC CATCAGCCTC GCCTTGGTGC	180
TCCTCGCCCT CTGCACCCGG CCTGCTACGG GCCAGGACTG CAGCGCGCAA TGTCAGTGCG	240
CAGCCGAAGC AGCGCCGCAC TGCCCCGCCG GCGTGAGCCT GGTGCTGGAC GGCTGCGGCT	300
GCTGCCGCGT CTGCGCCAAG CAGCTGGGAG AACTGTGTAC GGAGCGTGAC CCCTGCGACC	360
CACACAAGGG CCTCTTCTGC GATTTCGGCT CCCCCGCCAA CCGCAAGATT GGAGTGTGCA	420
CTGCCAAAGA TGGTGACCC TGTGTCTTCG GTGGGTGCGT GTACCGCAGC GGTGAGTCCT	480
TCCAAAGCAG CTGCAATAC CAATGCACTT GCCTGGATGG GGCCGTGGGC TGCCTGCCCC	540
TATGCAGCAT GGACGTGCGC CTGCCCAGCC CTGACTGCCC CTTCCCGAGA AGGGTCAAGC	600
TGCTTGGGAA ATGCTGCAAG GAGTGGGTGT GTGACGAGCC CAAGGACCGC ACAGCAGTTG	660



GCCCTGCCCT AGCTGCCTAC CGACTGGAAG ACACATTTGG CCCAGACCCA ACTATGATGC	720
GAGCCAACTG CCTGGTCCAG ACCACAGAGT GGAGCGCCTG TTCTAAGACC TGTGGAATGG	780
GCATCTCCAC CCGAGTTACC AATGACAATA CCTTCTGCAG ACTGGAGAAG CAGAGCCGCC	840
TCTGCATGGT CAGGCCCTGC GAAGCTGACC TGGAGGAAAA CATTAGAAG GGCAAAAAGT	900
GCATCCGGAC ACCTAAAATC GCCAAGCCTG TCAAGTTTGA GCTTCTGGC TGCACCACTG	960
TGAAGACATA CAGGGCTAAG TTCTGCGGGG TGTGCACAGA CGGCCCTGC TGCACACCGC	1020
ACAGAACCAC CACTCTGCCA GTGGAGTTCA AATGCCCCGA TGGCGAGATC ATGAAAAAGA	1080
ATATGATGTT CATCAAGACC TGTGCCTGCC ATTACAACTG TCCTGGGGAC AATGACATCT	1140
TTGAGTCCCT GTACTACAGG AAGATGTACG GAGACATGGC GTAAAGCCAG GAAGTAAGGG	1200
ACACGAACTC ATTAGACTAT AACTTGAAGT GAGTTGCATC TCATTTTCTT CTGTAAAAAC	1260
AATTACAGTA GCACATTAAT TTAAATCTGT GTTTTAACT ACCGTGGGAG GAACTATCCC	1320
ACCAAAGTGA GAACGTTATG TCATGGCCAT ACAAGTAGTC TGTCAACCTC AGACACTGGT	1380
TTGAGACAG TTTACACTTG ACAGTTGTTT ATTAGCGCAC AGTGCCAGAA CGCACACTGA	1440
GGTGAGTCTC CTGGAACAGT GGAGATGCCA GGAGAAAGAA AGACAGGTAC TAGCTGAGGT	1500
TATTTTAAAA GCAGCAGTGT GCCTACTTTT TGGAGTGTA CCGGGGAGGG AAATTATAGC	1560
ATGCTTGCAG ACAGACCTGC TCTAGCGAGA GCTGAGCATG TGTCTCCAC TAGATGAGGC	1620
TGAGTCCAGC TGTTCTTTAA GAACAGCAGT TTCAGCCTCT GACCATTCTG ATTCCAGTGA	1680
CACTTGTGAG GAGTCAGAGC CTTGTCTGTT AGACTGGACA GCTTGTGGCA AGTAAGTTTG	1740
CCTGTAACAA GCCAGATTTT TATTGATATT GTAAATATTG TGGATATATA TATATATATA	1800
TATATTTGTA CAGTTATCTA AGTTAATTTA AAGTCATTG TTTTGTGTTT AAGTGCTTTT	1860
GGGATTTTAA ACTGATAGCC TCAAACTCCA AACACCATAG GTAGGACACG AAGCTTATCT	1920
GTGATTCAAA ACAAAGGAGA TACTGCAGTG GGAATTGTGA CCTGAGTGAC TCTCTGTCAG	1980
AACAAACAAA TGCTGTGCAG GTGATAAAGC TATGTATTGG AAGTCAGATT TCTAGTAGGA	2040
AATGTGGTCA AATCCCTGTT GGTGAACAAA TGGCCTTTAT TAAGAAATGG CTGGCTCAGG	2100
GTAAGGTCCG ATTCCTACCA GGAAGTGCTT GCTGCTTCTT TGATTATGAC TGGTTTGGGG	2160
TGGGGGGCAG TTTATTTGTT GAGAGTGTGA CCAAAAGTTA CATGTTTGCA CCTTTCTAGT	2220
TGAAAATAAA GTATATATAT ATTTTATA TGAAAAAAA GGAATTC	2267

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 348 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: misc feature

(D) OTHER INFORMATION: "Fisp12 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Leu Ala Ser Val Ala Gly Pro Ile Ser Leu Ala Leu Val Leu Leu
 1           5           10           15
Ala Leu Cys Thr Arg Pro Ala Thr Gly Gln Asp Cys Ser Ala Gln Cys
 20           25           30
Gln Cys Ala Ala Glu Ala Ala Pro His Cys Pro Ala Gly Val Ser Leu
 35           40           45
Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu Gly
 50           55           60
Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu Phe
 65           70           75           80
Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr Ala
 85           90           95
Lys Asp Gly Ala Pro Cys Val Phe Gly Gly Ser Val Tyr Arg Ser Gly
100           105           110
Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp Gly
115           120           125
Ala Val Gly Cys Val Pro Leu Cys Ser Met Asp Val Arg Leu Pro Ser
130           135           140
Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys Cys
145           150           155           160
Lys Glu Trp Val Cys Asp Glu Pro Lys Asp Arg Thr Ala Val Gly Pro
165           170           175
Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro Thr
180           185           190
Met Met Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala Cys
195           200           205
Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn
210           215           220
Thr Phe Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro
225           230           235           240
Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile
245           250           255
Arg Thr Pro Lys Ile Ala Lys Pro Val Lys Phe Glu Leu Ser Gly Cys
260           265           270
Thr Ser Val Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr Asp
275           280           285
Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu Phe
290           295           300

```

Lys Cys Pro Asp Gly Glu Ile Met Lys Lys Asn Met Met Phe Ile Lys  
 305 310 315 320  
 Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe Glu  
 325 330 335  
 Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala  
 340 345

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2075 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (D) OTHER INFORMATION: "CTGF cDNA coding sequence"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

CCCCGCCGAC AGCCCCGAGA CGACAGCCCG GCGCGTCCCG GTCCCCACCT CCGACCACCG      60
CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCCGCCACCG CGCCCTCCGC TCCGCCGCA      120
GTGCCAACCA TGACCGCCGC CAGTATGGGC CCCGTCCGCG TCGCCTTCGT GGTCTCTCTC      180
GCCCTCTGCA GCCGGCCGGC CGTEGGCCAG AACTGCAGCG GGCCGTGCCG GTGCCCGGAC      240
GAGCCGGCGC CGCGCTGCCC GGCGGGCGTG AGCCTCGTGC TGGACGGCTG CGGCTGCTGC      300
CGCGTCTGCG CCAAGCAGCT GGGCGAGCTG TGACCCGAGC GCGACCCCTG CGACCCGCAC      360
AAGGGCCTCT TCTGTGACTT CGGCTCCCCG GCCAACCACA AGATCGGCGT GTGCACCGCC      420
AAAGATGGTG CTCCCTGCAT CTTCCGTGGT ACGGTGTACC GCAGCGGAGA GTCCTTCCAG      480
AGCAGCTGCA AGTACCAAGT CACGTGCCTG GACGGGGCGG TGGGCTGCAT GCCCCTGTGC      540
AGCATGGACG TTCGTCTGCC CAGCCCTGAC TGCCCTTCC CGAGGAGGGT CAAGCTGCCC      600
GGGAAATGCT GCGAGGAGTG GGTGTGTGAC GAGCCCAAGG ACCAAACCGT GGTGGGCCT      660
GCCCTCGCGG CTTACCGACT GGAAGACACG TTTGGCCAG ACCCAACTAT GATTAGAGCC      720
AACTGCCTGG TCCAGACCAC AGAGTGGAGC GCCTGTTCCT AGACCTGTGG GATGGGCATC      780
TCCACCCGGG TTACCAATGA CAACGCCTCC TGCAGGCTAG AGAAGCAGAG CCGCCTGTGC      840
ATGGTCAGGC CTTGCGAAGC TGACCTGGAA GAGAACAATTA AGAAGGGCAA AAAGTGCATC      900
CGTACTCCCA AAATCTCCAA GCCTATCAAG TTTGAGCTTT CTGGCTGCAC CAGCATGAAG      960
ACATACCGAG CTAAATTCTG TGGAGTATGT ACCGACGGCC GATGCTGCAC CCCCCACAGA     1020
ACCACCACCC TGCCGGTGGG GTTCAAGTGC CCTGACGGCG AGGTCATGAA GAAGAACATG     1080
ATGTTTCATCA AGACCTGTGC CTGCCATTAC AACTGTCCCG GAGACAATGA CATCTTTGAA     1140

```

TCGCTGTACT ACAGGAAGAT GTACGGAGAC ATGGCATGAA GCCAGAGAGT GAGAGACATT	1200
AACTCATTAG ACTGGAACCT GAACTGATTC ACATCTCATT TTTCCGTAAA AATGATTTCA	1260
GTAGCACAAG TTATTTAAAT CTGTTTTTCT AACTGGGGGA AAAGATTCCC ACCCAATTCA	1320
AAACATTGTG CCATGTCAAA CAAATAGTCT ATCTTCCCA GACACTGGTT TGAAGAATGT	1380
TAAGACTTGA CAGTGGAACT ACATTAGTAC ACAGCACCAG AATGTATATT AAGGTGTGGC	1440
TTTAGGAGCA GTGGGAGGGT ACCGGCCCCG TTAGTATCAT CAGATCGACT CTTATACGAG	1500
TAATATGCCT GCTATTTGAA GTGTAATTGA GAAGGAAAAT TTTAGCGTGC TCACTGACCT	1560
GCCTGTAGCC CCAGTGACAG CTAGGATGTG CATTCTCCAG CCATCAAGAG ACTGAGTCAA	1620
GTGTTCCTT AAGTCAGAAC AGCAGACTCA GCTCTGACAT TCTGATTCGA ATGACACTGT	1680
TCAGGAATCG GAATCCTGTC GATTAGACTG GACAGCTTGT GGCAAGTGAA TTGCCTGTA	1740
ACAAGCCAGA TTTTITAAAA TTTATATTGT AAATATTGTG TGTGTGTGTG TGTGTGTATA	1800
TATATATATA TATGTACAGT TATCTAAGTT AATTTAAAGT TGTGTGTGCC TTTTATTTT	1860
TGTTTTTAAT GCTTTGATAT TTCAATGTTA GCCTCAATTT CTGAACACCA TAGGTAGAAT	1920
GTAAAGCTTG TCTGATCGTT CAAAGCATGA AATGGATACT TATATGGAAA TTCTGCTCAG	1980
ATAGAATGAC AGTCCGTCOA AACAGATTGT TTGCAAAGGG GAGGCATCAG TGTCTTGGCA	2040
GGCTGATTTT TAGGTAGGAA ATGTGGTAGC TCACG	2075

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (D) OTHER INFORMATION: "CTGF amino acid sequence"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu	
1 5 10 15	
Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro	
20 25 30	
Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser	
35 40 45	
Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu	
50 55 60	
Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu	
65 70 75 80	

Phe	Cys	Asp	Phe	Gly	Ser	Pro	Ala	Asn	Arg	Lys	Ile	Gly	Val	Cys	Thr
				85					90					95	
Ala	Lys	Asp	Gly	Ala	Pro	Cys	Ile	Phe	Gly	Gly	Thr	Val	Tyr	Arg	Ser
			100					105					110		
Gly	Glu	Ser	Phe	Gln	Ser	Ser	Cys	Lys	Tyr	Gln	Cys	Thr	Cys	Leu	Asp
		115					120					125			
Gly	Ala	Val	Gly	Cys	Met	Pro	Leu	Cys	Ser	Met	Asp	Val	Arg	Leu	Pro
		130				135					140				
Ser	Pro	Asp	Cys	Pro	Phe	Pro	Arg	Arg	Val	Lys	Leu	Pro	Gly	Lys	Cys
145					150					155					160
Cys	Glu	Glu	Trp	Val	Cys	Asp	Glu	Pro	Lys	Asp	Gln	Thr	Val	Val	Gly
			165					170						175	
Pro	Ala	Leu	Ala	Ala	Tyr	Arg	Leu	Glu	Asp	Thr	Phe	Gly	Pro	Asp	Pro
			180					185					190		
Thr	Met	Ile	Arg	Ala	Asn	Cys	Leu	Val	Gln	Thr	Thr	Glu	Trp	Ser	Ala
		195					200					205			
Cys	Ser	Lys	Thr	Cys	Gly	Met	Gly	Ile	Ser	Thr	Arg	Val	Thr	Asn	Asp
		210				215					220				
Asn	Ala	Ser	Cys	Arg	Leu	Glu	Lys	Gln	Ser	Arg	Leu	Cys	Met	Val	Arg
225					230					235					240
Pro	Cys	Glu	Ala	Asp	Leu	Glu	Glu	Asn	Ile	Lys	Lys	Gly	Lys	Lys	Cys
				245					250					255	
Ile	Arg	Thr	Pro	Lys	Ile	Ser	Lys	Pro	Ile	Lys	Phe	Glu	Leu	Ser	Gly
			260					265					270		
Cys	Thr	Ser	Met	Lys	Thr	Tyr	Arg	Ala	Lys	Phe	Cys	Gly	Val	Cys	Thr
		275					280					285			
Asp	Gly	Arg	Cys	Cys	Thr	Pro	His	Arg	Thr	Thr	Thr	Leu	Pro	Val	Glu
		290				295						300			
Phe	Lys	Cys	Pro	Asp	Gly	Glu	Val	Met	Lys	Lys	Asn	Met	Met	Phe	Ile
305					310					315					320
Lys	Thr	Cys	Ala	Cys	His	Tyr	Asn	Cys	Pro	Gly	Asp	Asn	Asp	Ile	Phe
				325					330					335	
Glu	Ser	Leu	Tyr	Tyr	Arg	Lys	Met	Tyr	Gly	Asp	Met	Ala			
			340					345							

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGATCTGT GACGAGCCCA AGGAC

25

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGAATTCGA CCAGGCAGTT GGCTCG

26

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGGATCCTG TGATGAAGAC AGCATT

26

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGAATTCAA CGATGCATT CTGGCC

26

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp  
1 5 10 15  
Cys Ser Lys Thr Gln  
20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val Gly Cys  
1 5 10 15  
Ile Pro Leu Cys Pro  
20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser Cys Gly  
1 5 10 15  
Thr Gly Ile Ser Thr Arg Val Thr  
20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys Arg Leu Val Lys  
1 5 10 15  
Glu Thr Arg Ile Cys Glu Val Arg Pro Cys  
20 25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys Cys Thr Pro Leu Gln  
1 5 10 15  
Thr Arg Thr Val Lys  
20



**This Page is Inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record**

**BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ **BLACK BORDERS**
- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☐ **FADED TEXT OR DRAWING**
- ☒ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☒ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER: \_\_\_\_\_**

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.**